Mr. Gordon Allen, 155 Corona Avanue, Pelham 65, N.Y.

Dear Gordon-

As you can see from the letterhead, Esther and I are visiting California this supper, which accounts for the delay in my reply to your letters which I have just received. Right now, in fact, we are at Mather, where Dobzhansky has set up his collecting stations, and Stebbins is conducting a field trip in plant taxonomy and evolution. We are returning shortly to Berkeley, at the above address.

Of your three proposals for elaborating on the linkage analysis, your first seems the soundest. I don't understand the second "maps obtained when small amounts of the selected factors are present". The third (comparison of single with odd n-ple crossover classes) would be very involved conscially if interference (positive and negative) must be considered.

I am still convinced that you should publish your significant results. Newcombe just now sent an MS showing crossover data among prototrophs from such crosses as W-677 ST x 58-161, with and without further selection with streptomycin (to collect the rare Sr prototrophs). He thinks he can simply map 3, Mal, etc. to the left of M, and explain away additional discordancies as "negative interference" / I mentioned, briofily, your line of research, but suggested that he consult you for details. You once mentioned that nutritionally complementary selections (not necessarily associated reciprocals) failed to show complementary segregation for Mal. If this is verified, then any simple mapping with prototrophs becomes vitiated. at least for the present. Newcombe also has not encountered the anomalous effect (or tather lack of it) of B, on these segregations which would appear to necessitate placing the Bl locus on a separate, third branch from Mal, S, otc., on the one side and Lac, V1 on the other. Negative interference does not seem to me to explain anything, and I suspect that a good many people might be more inclined to reject the concept of lineality as a proven mechanism in E. coli, rather than to accept this modification. Your data would really help to clear the air considerably, if they are extensive enough for you to be willing to publish them.

Before closing, may I refer to any part of your unpublished work in a resume of (part of) bacterial genetics to be used as an address at the Columbus Conetics Society meetings. It might be best if you would mentic specifically what approaches and conclusions I may cite, if any. If pos I would like to have this within a month, although later revision (til 15) is possible. Thanks very much.

Sincerely,